

PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/018,924

DATE: 01/17/2002

TIME: 07:15:17

Input Set : A:\S0042PCTSEQ.txt

Output Set: N:\CRF3\01172002\J018924.raw

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2 <110> APPLICANT: Shionogi & Co., Ltd

4 <120> TITLE OF INVENTION: Composition for promoting passive extension of bladder smooth muscle

W--> 5 <130> FILE REFERENCE: S0042PCT

C--> 7 <140> CURRENT APPLICATION NUMBER: US/10/018,924

C--> 8 <141> CURRENT FILING DATE: 2001-12-19

9 <150> PRIOR APPLICATION NUMBER: JP P1999-177549

10 <151> PRIOR FILING DATE: 1999-06-23

12 <160> NUMBER OF SEQ ID NOS: 6

14 <170> SOFTWARE: PatentIn Ver. 2.0

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 1457

18 <212> TYPE: DNA

19 <213> ORGANISM: Homo sapiens

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (165)..(719)

25 <220> FEATURE:

W- 26 <221> NAME/KEY: mat peptide

27 <222> LOCATION: (447)..(602)

29 <400> SEQUENCE: 1

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32 cttggacttc ggagttttgc cattgccagt gggacgtctg agactttctc cttcaagtac 120
34 ttggcagatc actctcttag cagggtctgc gcttcgcagc cggg atg aag ctg gtt 176
35                                     Met Lys Leu Val
37 tcc gtc gcc ctg atg tac ctg ggt tcg ctc gcc ttc cta ggc gct gac 224
38 Ser Val Ala Leu Met Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp
39 -90                               -85                               -80                               -75
41 acc gct cgg ttg gat gtc gcg tcg gag ttt cga aag aag tgg aat aag 272
42 Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys Lys Trp Asn Lys
43                               -70                               -65                               -60
45 tgg gct ctg agt cgt ggg aag agg gaa ctg cgg atg tcc agc agc tac 320
46 Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met Ser Ser Ser Tyr
47                               -55                               -50                               -45
49 ccc acc ggg ctc gct gac gtg aag gcc ggg cct gcc cag acc ctt att 368
50 Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala Gln Thr Leu Ile
51                               -40                               -35                               -30
53 cgg ccc cag gac atg aag ggt gcc tct cga agc ccc gaa gac agc agt 416
54 Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro Glu Asp Ser Ser
55                               -25                               -20                               -15
57 ccg gat gcc gcc cgc atc cga gtc aag cgc tac cgc cag agc atg aac 464
58 Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn
59 -10                               -5                               -1                               1                               5
61 aac ttc cag ggc ctc cgg agc ttt ggc tgc cgc ttc ggg acg tgc acg 512
62 Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr
63                               10                               15                               20
65 gtg cag aag ctg gca cac cag atc tac cag ttc aca gat aag gac aag 560
66 Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys

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69 gac aac gtc gcc ccc agg agc aag atc agc ccc cag ggc tac ggc cgc 608
70 Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg
71          40          45          50
73 cgg cgc cgg cgc tcc ctg ccc gag gcc ggc ccg ggt cgg act ctg gtg 656
74 Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly Arg Thr Leu Val
75 55          60          65          70
77 tct tct aag cca caa gca cac ggg gct cca gcc ccc ccg agt gga agt 704
78 Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro Pro Ser Gly Ser
79          75          80          85
81 gct ccc cac ttt ctt taggatttag gcgcccattg tacaaggaat agtcgcgcaa 759
82 Ala Pro His Phe Leu
83          90
85 gcatcccgct ggtgctctcc gggacgaagg acttcccgag cgggtgtgggg accgggctct 819
87 gacagccctg cggagaccct gagtccggga ggcaccgtcc ggcggcgagc tctggctttg 879
89 caagggcccc tccttctggg ggcttcgctt ccttagcctt gctcaggtgc aagtgcctca 939
91 gggggcgggg tgcagaagaa tccgagtgtt tgccaggctt aaggagagga gaaactgaga 999
93 aatgaatget gagacccccg gagcaggggt ctgagccaca gccgtgctcg cccacaaact 1059
95 gattttctcac ggcgtgtcac cccaccaggg cgcaagcctc actattactt gaactttcca 1119
97 aaacctaaag aggaaaagtg caatgcgtgt tgtacataca gaggtaacta tcaatattta 1179
99 agtttgttgc tgtcaagatt tttttgttaa cttcaaatat agagatattt ttgtacgtta 1239
101 tatattgtat taagggcatt ttaaagcaa ttatattgtc ctcccctatt ttaagacgtg 1299
103 aatgtctcag cgaggtgtaa agttgttcgc cgcgtggaat gtgagtgtgt ttgtgtgcat 1359
105 gaaagagaaa gactgattac ctctgtgtg gaagaaggaa acaccgagtc tctgtataat 1419
107 ctattttacat aaaatgggtg atatgcgaac agcaaacc 1457
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111 <211> LENGTH: 185
112 <212> TYPE: PRT
113 <213> ORGANISM: Homo sapiens
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119 Leu Gly Ala Asp Thr Ala Arg Leu Asp Val Ala Ser Glu Phe Arg Lys
120          -75          -70          -65
122 Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Met
123          -60          -55          -50
125 Ser Ser Ser Tyr Pro Thr Gly Leu Ala Asp Val Lys Ala Gly Pro Ala
126          -45          -40          -35
128 Gln Thr Leu Ile Arg Pro Gln Asp Met Lys Gly Ala Ser Arg Ser Pro
129 -30          -25          -20          -15
131 Glu Asp Ser Ser Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
132          -10          -5          -1 1
134 Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
135          5          10          15
137 Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
138          20          25          30
140 Asp Lys Asp Lys Asp Asn Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
141 35          40          45          50
143 Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu Pro Glu Ala Gly Pro Gly

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144          55          60          65
146 Arg Thr Leu Val Ser Ser Lys Pro Gln Ala His Gly Ala Pro Ala Pro
147          70          75          80
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154 <211> LENGTH: 1493
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156 <213> ORGANISM: Sus scrofa
158 <220> FEATURE:
159 <221> NAME/KEY: CDS
160 <222> LOCATION: (148)..(711)
162 <220> FEATURE:
W--> 163 <221> NAME/KEY: mat peptide
164 <222> LOCATION: (430)..(585)
166 <400> SEQUENCE: 3
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169 tgccactgcc agagggacgt ctcagacttc atcttcccaa atcttggcag atcaccct 120
171 tagcagggtc tgcacatctc agccggg atg aag ctg gtt ccc gta gcc ctc atg 174
172 Met Lys Leu Val Pro Val Ala Leu Met
173 -90
175 tac ctg ggc tcg ctc gcc ttc ctg ggc gct gac aca gct cgg ctc gac 222
176 Tyr Leu Gly Ser Leu Ala Phe Leu Gly Ala Asp Thr Ala Arg Leu Asp
177 -85 -80 -75 -70
179 gtg gcg gca gag ttc cga aag aaa tgg aat aag tgg gct cta agt cgt 270
180 Val Ala Ala Glu Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu Ser Arg
181 -65 -60 -55
183 gga aaa aga gaa ctt cgg ctg tcc agc agc tac ccc acc ggg atc gcc 318
184 Gly Lys Arg Glu Leu Arg Leu Ser Ser Ser Tyr Pro Thr Gly Ile Ala
185 -50 -45 -40
187 gac ttg aag gcc ggg cct gcc cag act gtc att cgg ccc cag gat gtg 366
188 Asp Leu Lys Ala Gly Pro Ala Gln Thr Val Ile Arg Pro Gln Asp Val
189 -35 -30 -25
191 aag ggc tcc tct cgc agc ccc cag gcc agc att ccg gat gca gcc cgc 414
192 Lys Gly Ser Ser Arg Ser Pro Gln Ala Ser Ile Pro Asp Ala Ala Arg
193 -20 -15 -10
195 atc cga gtc aag cgc tac cgc cag agt atg aac aac ttc cag ggc ctg 462
196 Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Asn Phe Gln Gly Leu
197 -5 -1 1 5 10
199 cgg agc ttc ggc tgt cgc ttt ggg acg tgc acc gtg cag aag ctg gcg 510
200 Arg Ser Phe Gly Cys Arg Phe Gly Thr Cys Thr Val Gln Lys Leu Ala
201 15 20 25
203 cac cag atc tac cag ttc acg gac aaa gac aag gac ggc gtc gcc ccc 558
204 His Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Val Ala Pro
205 30 35 40
207 cgg agc aag atc agc ccc cag ggc tac ggc cgc cgg cgc cga cgc tct 606
208 Arg Ser Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Ser
209 45 50 55
211 ctg ccc gaa gcc agc ctg ggc cgg act ctg agg tcc cag gag cca cag 654

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212 Leu Pro Glu Ala Ser Leu Gly Arg Thr Leu Arg Ser Gln Glu Pro Gln
213 60 65 70 75
215 gcg cac ggg gcc ccg gcc tcc ccg gcg cat caa gtg ctc gcc act ctc 702
216 Ala His Gly Ala Pro Ala Ser Pro Ala His Gln Val Leu Ala Thr Leu
217 80 85 90
219 ttt agg att taggcgccta ctgtggcagc agcgaacagt cgcgcgatgca 751
220 Phe Arg Ile
222 tcatgccggc gcttcctggg gcgggggggct tcccgaggcc gagcccctca gcggctgggg 811
224 cccgggcaga gacagcattg agagaccgag agtccgggag gcacagacca gcggcgagcc 871
226 ctgcattttc aggaacccgt cctgcttgga ggcagtgttc tcttcggctt aatccagccc 931
228 ggggtcccggt gtgggggtgg aggggtgcaga ggaatccaaa ggagtgtcat ctgccaggct 991
230 cacggagagg agaaactgcg aagtaaattgc ttagaccccc aggggcaagg gtctgagcca 1051
232 ctgccgtgcc gccacaaaac tgattttctga aggggaataa cccaacagg gcgcaagcct 1111
234 cactattact tgaactttcc aaaacctaga gagggaaagt gcaatgtatg ttgtatataa 1171
236 agaggtaact atcaatatct aagtttggtg ctgtcaagat ttttttttgt aacttcaaat 1231
238 atagagatat tttgtacgt tatatatgtt attaagggca ttttaaaaca attgtattgt 1291
240 tcccctcccc tctattttta tatgtgaatg tctcagcgag gtgtaacatt gtttgctgcg 1351
242 cgaaatgtga gagtgtgtgt gtgtgtgtgc gtgaaagaga gtctggatgc ctcttgggga 1411
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246 aaaccaataa actgtctcaa tg 1493
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250 <211> LENGTH: 188
251 <212> TYPE: PRT
252 <213> ORGANISM: Sus scrofa
254 <400> SEQUENCE: 4
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259 -75 -70 -65
261 Lys Trp Asn Lys Trp Ala Leu Ser Arg Gly Lys Arg Glu Leu Arg Leu
262 -60 -55 -50
264 Ser Ser Ser Tyr Pro Thr Gly Ile Ala Asp Leu Lys Ala Gly Pro Ala
265 -45 -40 -35
267 Gln Thr Val Ile Arg Pro Gln Asp Val Lys Gly Ser Ser Arg Ser Pro
268 -30 -25 -20 -15
270 Gln Ala Ser Ile Pro Asp Ala Ala Arg Ile Arg Val Lys Arg Tyr Arg
271 -10 -5 -1 1
273 Gln Ser Met Asn Asn Phe Gln Gly Leu Arg Ser Phe Gly Cys Arg Phe
274 5 10 15
276 Gly Thr Cys Thr Val Gln Lys Leu Ala His Gln Ile Tyr Gln Phe Thr
277 20 25 30
279 Asp Lys Asp Lys Asp Gly Val Ala Pro Arg Ser Lys Ile Ser Pro Gln
280 35 40 45 50
282 Gly Tyr Gly Arg Arg Arg Arg Ser Leu Pro Glu Ala Ser Leu Gly
283 55 60 65
285 Arg Thr Leu Arg Ser Gln Glu Pro Gln Ala His Gly Ala Pro Ala Ser
286 70 75 80
288 Pro Ala His Gln Val Leu Ala Thr Leu Phe Arg Ile
289 85 90

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 293 <211> LENGTH: 1376
 294 <212> TYPE: DNA
 295 <213> ORGANISM: Rattus norvegicus
 297 <220> FEATURE:
 298 <221> NAME/KEY: CDS
 299 <222> LOCATION: (154)..(708)
 301 <220> FEATURE:
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 303 <222> LOCATION: (433)..(582)
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 308 ggttttgcg ctgtcagaag gacgtctcgg actttctgct tcaagtgtt gacaactcac 120
 310 cttttcagca gggatcggga gcatcgctac aga atg aag ctg gtt tcc atc gcc 174
 311 Met Lys Leu Val Ser Ile Ala
 312 -90
 314 ctg atg tta ttg ggt tcg ctc gcc gtt ctc ggc gcg gac acc gca cgg 222
 315 Leu Met Leu Leu Gly Ser Leu Ala Val Leu Gly Ala Asp Thr Ala Arg
 316 -85 -80 -75
 318 ctc gac act tcc tcg cag ttc cga aag aag tgg aat aag tgg gcg cta 270
 319 Leu Asp Thr Ser Ser Gln Phe Arg Lys Lys Trp Asn Lys Trp Ala Leu
 320 -70 -65 -60 -55
 322 agt cgt ggg aag agg gaa cta caa gcg tcc agc agc tac cct acg ggg 318
 323 Ser Arg Gly Lys Arg Glu Leu Gln Ala Ser Ser Ser Tyr Pro Thr Gly
 324 -50 -45 -40
 326 ctc gtt gat gag aag aca gtc ccg acc cag act ctt ggg ctc cag gac 366
 327 Leu Val Asp Glu Lys Thr Val Pro Thr Gln Thr Leu Gly Leu Gln Asp
 328 -35 -30 -25
 330 aag cag agc acg tct agc acc cca caa gcc agc act cag agc aca gcc 414
 331 Lys Gln Ser Thr Ser Ser Thr Pro Gln Ala Ser Thr Gln Ser Thr Ala
 332 -20 -15 -10
 334 cac att cga gtc aaa cgc tac cgc cag agc atg aac cag ggg tcc cgc 462
 335 His Ile Arg Val Lys Arg Tyr Arg Gln Ser Met Asn Gln Gly Ser Arg
 336 -5 -1 1 5 10
 338 agc act gga tgc cgc ttt ggg acc tgc aca atg cag aaa ctg gct cac 510
 339 Ser Thr Gly Cys Arg Phe Gly Thr Cys Thr Met Gln Lys Leu Ala His
 340 15 20 25
 342 cag atc tac cag ttt aca gac aaa gac aag gac ggc atg gcc ccc aga 558
 343 Gln Ile Tyr Gln Phe Thr Asp Lys Asp Lys Asp Gly Met Ala Pro Arg
 344 30 35 40
 346 aac aag atc agc cct caa ggc tat ggc cgc cgg cgc cgg cgt tcc ctg 606
 347 Asn Lys Ile Ser Pro Gln Gly Tyr Gly Arg Arg Arg Arg Arg Ser Leu
 348 45 50 55
 350 cca gag gtc ctc cga gcc cgg act gtg gag tcc tcc cag gag cag aca 654
 351 Pro Glu Val Leu Arg Ala Arg Thr Val Glu Ser Ser Gln Glu Gln Thr
 352 60 65 70
 354 cac tca gct cca gcc tcc ccg gcg cac caa gac atc tcc aga gtc tct 702
 355 His Ser Ala Pro Ala Ser Pro Ala His Gln Asp Ile Ser Arg Val Ser
 356 75 80 85 90

